PCT09

```
        RAW SEQUENCE LISTING                    DATE: 02/14/2002
        PATENT APPLICATION:  US/09/763,334      TIME: 15:11:47

        Input Set : A:\6523-020-999.txt
        Output Set: N:\CRF3\02142002\I763334.raw
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 4  <110> APPLICANT: Yale University
 6  <120> TITLE OF INVENTION: TREATMENT AND PREVENTION OF CANCER AND PITUITARY
 7        DISORDERS WITH LATS PROTEINS, DERIVATIVES AND
 8        FRAGMENTS, AND LATS KNOCK-OUT ANIMAL MODELS
10  <130> FILE REFERENCE: 6523-020-999
12  <140> CURRENT APPLICATION NUMBER: 09/763,334
13  <141> CURRENT FILING DATE: 1999-08-18
15  <160> NUMBER OF SEQ ID NOS: 9
17  <170> SOFTWARE: PatentIn Ver. 2.0
19  <210> SEQ ID NO: 1
20  <211> LENGTH: 3984
21  <212> TYPE: DNA
22  <213> ORGANISM: Homo sapiens
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26  <222> LOCATION: (231)..(3620)
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33  acagtcctgg ggacttcctt gaaggatcat tttcactttt gctcagaaga aagctctgga 180
35  tctatcaaat aaagaagtcc ttcgtgtggg ctacatatat agatgttttc atg aag    236
36                                                            Met Lys
37                                                             1
39  agg agt gaa aag cca gaa gga tat aga caa atg agg cct aag acc ttt   284
40  Arg Ser Glu Lys Pro Glu Gly Tyr Arg Gln Met Arg Pro Lys Thr Phe
41          5               10                  15
43  cct gcc agt aac tat act gtc agt agc cgg caa atg tta caa gaa att   332
44  Pro Ala Ser Asn Tyr Thr Val Ser Ser Arg Gln Met Leu Gln Glu Ile
45          20              25                  30
47  cgg gaa tcc ctt agg aat tta tct aaa cca tct gat gct gct aag gct   380
48  Arg Glu Ser Leu Arg Asn Leu Ser Lys Pro Ser Asp Ala Ala Lys Ala
49  35              40                  45                  50
51  gag cat aac atg agt aaa atg tca acc gaa gat cct cga caa gtc aga   428
52  Glu His Asn Met Ser Lys Met Ser Thr Glu Asp Pro Arg Gln Val Arg
53                  55                  60                  65
55  aat cca ccc aaa ttt ggg acg cat cat aaa gcc ttg cag gaa att cga   476
56  Asn Pro Pro Lys Phe Gly Thr His His Lys Ala Leu Gln Glu Ile Arg
57              70                  75                  80
59  aac tct ctg ctt cca ttt gca aat gaa aca aat tct tct cgg agt act   524
60  Asn Ser Leu Leu Pro Phe Ala Asn Glu Thr Asn Ser Ser Arg Ser Thr
61          85                  90                  95
63  tca gaa gtt aat cca caa atg ctt caa gac ttg caa gct gct gga ttt   572
64  Ser Glu Val Asn Pro Gln Met Leu Gln Asp Leu Gln Ala Ala Gly Phe
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65      100                    105                    110
67 gat gag gat atg gtt ata caa gct ctt cag aaa act aac aac aga agt    620
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69 115                    120                    125                    130
71 ata gaa gca gca att gaa ttc att agt aaa atg agt tac caa gat cct    668
72 Ile Glu Ala Ala Ile Glu Phe Ile Ser Lys Met Ser Tyr Gln Asp Pro
73                    135                    140                    145
75 cga cga gag cag atg gct gca gca gct gcc aga cct att aat gcc agc    716
76 Arg Arg Glu Gln Met Ala Ala Ala Ala Ala Arg Pro Ile Asn Ala Ser
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79 atg aaa cca ggg aat gtg cag caa tca gtt aac cgc aaa cag agc tgg    764
80 Met Lys Pro Gly Asn Val Gln Gln Ser Val Asn Arg Lys Gln Ser Trp
81          165                    170                    175
83 aaa ggt tct aaa gaa tcc tta gtt cct cag agg cat ggc ccg cca cta    812
84 Lys Gly Ser Lys Glu Ser Leu Val Pro Gln Arg His Gly Pro Pro Leu
85      180                    185                    190
87 gga gaa agt gtg gcc tat cat tct gag agt ccc aac tca cag aca gat    860
88 Gly Glu Ser Val Ala Tyr His Ser Glu Ser Pro Asn Ser Gln Thr Asp
89 195                    200                    205                    210
91 gta gga aga cct ttg tct gga tct ggt ata tca gca ttt gtt caa gct    908
92 Val Gly Arg Pro Leu Ser Gly Ser Gly Ile Ser Ala Phe Val Gln Ala
93                    215                    220                    225
95 cac cct agc aac gga cag aga gtg aac ccc cca cca cca cct caa gta    956
96 His Pro Ser Asn Gly Gln Arg Val Asn Pro Pro Pro Pro Gln Val
97                    230                    235                    240
99 agg agt gtt act cct cca cca cct cca aga ggc cag act ccc cct cca    1004
100 Arg Ser Val Thr Pro Pro Pro Pro Arg Gly Gln Thr Pro Pro Pro
101          245                    250                    255
103 aga ggt aca act cca cct ccc cct tca tgg gaa cca aac tct caa aca    1052
104 Arg Gly Thr Thr Pro Pro Pro Pro Ser Trp Glu Pro Asn Ser Gln Thr
105      260                    265                    270
107 aag cgc tat tct gga aac atg gaa tac gta atc tcc cga atc tct cct    1100
108 Lys Arg Tyr Ser Gly Asn Met Glu Tyr Val Ile Ser Arg Ile Ser Pro
109 275                    280                    285                    290
111 gtc cca cct ggg gca tgg caa gag ggc tat cct cca cca cct ctc aac    1148
112 Val Pro Pro Gly Ala Trp Gln Glu Gly Tyr Pro Pro Pro Pro Leu Asn
113                    295                    300                    305
115 act tcc ccc atg aat cct cct aat caa gga cag aga ggc att agt tct    1196
116 Thr Ser Pro Met Asn Pro Pro Asn Gln Gly Gln Arg Gly Ile Ser Ser
117          310                    315                    320
119 gtt cct gtt ggc aga caa cca atc atc atg cag agt tct agc aaa ttt    1244
120 Val Pro Val Gly Arg Gln Pro Ile Ile Met Gln Ser Ser Ser Lys Phe
121          325                    330                    335
123 aac ttt cca tca ggg aga cct gga atg cag aat ggt act gga caa act    1292
124 Asn Phe Pro Ser Gly Arg Pro Gly Met Gln Asn Gly Thr Gly Gln Thr
125      340                    345                    350
127 gat ttc atg ata cac caa aat gtt gtc cct gct ggc act gtg aat cgg    1340
128 Asp Phe Met Ile His Gln Asn Val Val Pro Ala Gly Thr Val Asn Arg
129 355                    360                    365                    370
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131 cag cca cca cct cca tat cct ctg aca gca gct aat gga caa agc cct    1388
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133                 375                 380                 385
135 tct gct tta caa aca ggg gga tct gct gct cct tcg tca tat aca aat    1436
136 Ser Ala Leu Gln Thr Gly Gly Ser Ala Ala Pro Ser Ser Tyr Thr Asn
137                 390                 395                 400
139 gga agt att cct cag tct atg atg gtg cca aac aga aat agt cat aac    1484
140 Gly Ser Ile Pro Gln Ser Met Met Val Pro Asn Arg Asn Ser His Asn
141             405                 410                 415
143 atg gaa cta tat aac att agt gta cct gga ctg caa aca aat tgg cct    1532
144 Met Glu Leu Tyr Asn Ile Ser Val Pro Gly Leu Gln Thr Asn Trp Pro
145         420                 425                 430
147 cag tca tct tct gct cca gcc cag tca tcc ccg agc agt ggg cat gaa    1580
148 Gln Ser Ser Ser Ala Pro Ala Gln Ser Ser Pro Ser Ser Gly His Glu
149 435                 440                 445                 450
151 atc cct aca tgg caa cct aac ata cca gtg agg tca aat tct ttt aat    1628
152 Ile Pro Thr Trp Gln Pro Asn Ile Pro Val Arg Ser Asn Ser Phe Asn
153                 455                 460                 465
155 aac cca tta gga aat aga gca agt cac tct gct aat tct cag cct tct    1676
156 Asn Pro Leu Gly Asn Arg Ala Ser His Ser Ala Asn Ser Gln Pro Ser
157                 470                 475                 480
159 gct aca aca gtc act gca att aca cca gct cct att caa cag cct gtg    1724
160 Ala Thr Thr Val Thr Ala Ile Thr Pro Ala Pro Ile Gln Gln Pro Val
161             485                 490                 495
163 aaa agt atg cgt gta tta aaa cca gag cta cag act gct tta gca cct    1772
164 Lys Ser Met Arg Val Leu Lys Pro Glu Leu Gln Thr Ala Leu Ala Pro
165         500                 505                 510
167 aca cac cct tct tgg ata cca cag cca att caa act gtt caa ccc agt    1820
168 Thr His Pro Ser Trp Ile Pro Gln Pro Ile Gln Thr Val Gln Pro Ser
169 515                 520                 525                 530
171 cct ttt cct gag gga acc gct tca aat gtg act gtg atg cca cct gtt    1868
172 Pro Phe Pro Glu Gly Thr Ala Ser Asn Val Thr Val Met Pro Pro Val
173                 535                 540                 545
175 gct gaa gct cca aac tat caa gga cca cca cca ccc tac cca aaa cat    1916
176 Ala Glu Ala Pro Asn Tyr Gln Gly Pro Pro Pro Pro Tyr Pro Lys His
177             550                 555                 560
179 ctg ctg cac caa aac cca tct gtt cct cca tac gag tca atc agt aag    1964
180 Leu Leu His Gln Asn Pro Ser Val Pro Pro Tyr Glu Ser Ile Ser Lys
181             565                 570                 575
183 cct agc aaa gag gat cag cca agc ttg ccc aag gaa gat gag agt gaa    2012
184 Pro Ser Lys Glu Asp Gln Pro Ser Leu Pro Lys Glu Asp Glu Ser Glu
185         580                 585                 590
187 aag agt tat gaa aat gtt gat agt ggg gat aaa gaa aag aaa cag att    2060
188 Lys Ser Tyr Glu Asn Val Asp Ser Gly Asp Lys Glu Lys Lys Gln Ile
189 595                 600                 605                 610
191 aca act tca cct att act gtt agg aaa aac aag aaa gat gaa gag cga    2108
192 Thr Thr Ser Pro Ile Thr Val Arg Lys Asn Lys Lys Asp Glu Glu Arg
193                 615                 620                 625
195 agg gaa tct cgt att caa agt tat tct cct caa gca ttt aaa ttc ttt    2156
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196 Arg Glu Ser Arg Ile Gln Ser Tyr Ser Pro Gln Ala Phe Lys Phe Phe
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200 Met Glu Gln His Val Glu Asn Val Leu Lys Ser His Gln Gln Arg Leu
201             645             650             655
203 cat cgt aaa aaa caa tta gag aat gaa atg atg cgg gtt gga tta tct   2252
204 His Arg Lys Lys Gln Leu Glu Asn Glu Met Met Arg Val Gly Leu Ser
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207 caa gat gcc cag gat caa atg aga aag atg ctt tgc caa aaa gaa tct   2300
208 Gln Asp Ala Gln Asp Gln Met Arg Lys Met Leu Cys Gln Lys Glu Ser
209 675             680             685             690
211 aat tac atc cgt ctt aaa agg gct aaa atg gac aag tct atg ttt gtg   2348
212 Asn Tyr Ile Arg Leu Lys Arg Ala Lys Met Asp Lys Ser Met Phe Val
213             695             700             705
215 aag ata aag aca cta gga ata gga gca ttt ggt gaa gtc tgt cta gca   2396
216 Lys Ile Lys Thr Leu Gly Ile Gly Ala Phe Gly Glu Val Cys Leu Ala
217             710             715             720
219 aga aaa gta gat act aag gct ttg tat gca aca aaa act ctt cga aag   2444
220 Arg Lys Val Asp Thr Lys Ala Leu Tyr Ala Thr Lys Thr Leu Arg Lys
221     725             730             735
223 aaa gat gtt ctt ctt cga aat caa gtc gct cat gtt aag gct gag aga   2492
224 Lys Asp Val Leu Leu Arg Asn Gln Val Ala His Val Lys Ala Glu Arg
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227 gat atc ctg gct gaa gct gac aat gaa tgg gta gtt cgt cta tat tat   2540
228 Asp Ile Leu Ala Glu Ala Asp Asn Glu Trp Val Val Arg Leu Tyr Tyr
229 755             760             765             770
231 tca ttc caa gat aag gac aat tta tac ttt gta atg gac tac att cct   2588
232 Ser Phe Gln Asp Lys Asp Asn Leu Tyr Phe Val Met Asp Tyr Ile Pro
233             775             780             785
235 ggg ggt gat atg atg agc cta tta att aga atg ggc atc ttt cca gaa   2636
236 Gly Gly Asp Met Met Ser Leu Leu Ile Arg Met Gly Ile Phe Pro Glu
237             790             795             800
239 agt ctg gca cga ttc tac ata gca gaa ctt acc tgt gca gtt gaa agt   2684
240 Ser Leu Ala Arg Phe Tyr Ile Ala Glu Leu Thr Cys Ala Val Glu Ser
241         805             810             815
243 gtt cat aaa atg ggt ttt att cat aga gat att aaa cct gat aat att   2732
244 Val His Lys Met Gly Phe Ile His Arg Asp Ile Lys Pro Asp Asn Ile
245     820             825             830
247 ttg att gat cgt gat ggt cat att aaa ttg act gac ttt ggc ctc tgc   2780
248 Leu Ile Asp Arg Asp Gly His Ile Lys Leu Thr Asp Phe Gly Leu Cys
249 835             840             845             850
251 act ggc ttc aga tgg aca cac gat tct aag tac tat cag agt ggt gac   2828
252 Thr Gly Phe Arg Trp Thr His Asp Ser Lys Tyr Tyr Gln Ser Gly Asp
253             855             860             865
255 cat cca cgg caa gat agc atg gat ttc agt aat gaa tgg ggg gat ccc   2876
256 His Pro Arg Gln Asp Ser Met Asp Phe Ser Asn Glu Trp Gly Asp Pro
257             870             875             880
259 tca agc tgt cga tgt gga gac aga ctg aag cca tta gag cgg aga gct   2924
260 Ser Ser Cys Arg Cys Gly Asp Arg Leu Lys Pro Leu Glu Arg Arg Ala
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263 gca cgc cag cac cag cga tgt cta gca cat tct ttg gtt ggg act ccc   2972
264 Ala Arg Gln His Gln Arg Cys Leu Ala His Ser Leu Val Gly Thr Pro
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267 aat tat att gca cct gaa gtg ttg cta cga aca gga tac aca cag ttg   3020
268 Asn Tyr Ile Ala Pro Glu Val Leu Leu Arg Thr Gly Tyr Thr Gln Leu
269 915                   920                    925               930
271 tgt gat tgg tgg agt gtt ggt gtt att ctt ttt gaa atg ttg gtg gga   3068
272 Cys Asp Trp Trp Ser Val Gly Val Ile Leu Phe Glu Met Leu Val Gly
273             935                   940                    945
275 caa cct cct ttc ttg gca caa aca cca tta gaa aca caa atg aag gtt   3116
276 Gln Pro Pro Phe Leu Ala Gln Thr Pro Leu Glu Thr Gln Met Lys Val
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280 Ile Asn Trp Gln Thr Ser Leu His Ile Pro Pro Gln Ala Lys Leu Ser
281         965                   970                    975
283 cct gaa gct tct gat ctt att att aaa ctt tgc cga gga ccc gaa gat   3212
284 Pro Glu Ala Ser Asp Leu Ile Ile Lys Leu Cys Arg Gly Pro Glu Asp
285     980                   985                    990
287 cgc tta ggc aag aat ggt gct gat gaa ata aaa gct cat cca ttt ttt   3260
288 Arg Leu Gly Lys Asn Gly Ala Asp Glu Ile Lys Ala His Pro Phe Phe
289 995                   1000                  1005               1010
291 aaa aca att gac ttc tcc agt gac ctg aga cag cag tct gct tca tac   3308
292 Lys Thr Ile Asp Phe Ser Ser Asp Leu Arg Gln Gln Ser Ala Ser Tyr
293             1015                  1020                  1025
295 att cct aaa atc aca cac cca aca gat aca tca aat ttt gat cct gtt   3356
296 Ile Pro Lys Ile Thr His Pro Thr Asp Thr Ser Asn Phe Asp Pro Val
297             1030                  1035                  1040
299 gat cct gat aaa tta tgg agt gat gat aac gag gaa gaa aat gta aat   3404
300 Asp Pro Asp Lys Leu Trp Ser Asp Asp Asn Glu Glu Glu Asn Val Asn
301         1045                  1050                  1055
303 gac act ctc aat gga tgg tat aaa aat gga aag cat cct gaa cat gca   3452
304 Asp Thr Leu Asn Gly Trp Tyr Lys Asn Gly Lys His Pro Glu His Ala
305     1060                  1065                  1070
307 ttc tat gaa ttt acc ttc cga agg ttt ttt gat gac aat ggc tac cca   3500
308 Phe Tyr Glu Phe Thr Phe Arg Arg Phe Phe Asp Asp Asn Gly Tyr Pro
309 1075                  1080                  1085                  1090
311 tat aat tat ccg aag cct att gaa tat gaa tac att aat tca caa ggc   3548
312 Tyr Asn Tyr Pro Lys Pro Ile Glu Tyr Glu Tyr Ile Asn Ser Gln Gly
313             1095                  1100                  1105
315 tca gag cag cag tcg gat gaa gat gat caa aac aca ggc tca gag att   3596
316 Ser Glu Gln Gln Ser Asp Glu Asp Asp Gln Asn Thr Gly Ser Glu Ile
317             1110                  1115                  1120
319 aaa aat cgc gat cta gta tat gtt taacacacta gtaaataaat gtaatgagga   3650
320 Lys Asn Arg Asp Leu Val Tyr Val
321         1125                  1130
323 tttgtaaaag ggcctgaaat gcgaggtgtt ttgaggttct gagagtaaaa ttatgcaaat 3710
325 atgacagagc tatatatgtg tgctctgtgt acaatatttt attttcctaa attatgggaa 3770
327 atccttttaa aatgttaatt tattccagcc gtttaaatca gtatttagaa aaaaattgtt 3830
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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 02/14/2002
PATENT APPLICATION: US/09/763,334   TIME: 15:11:49

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1614 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1910 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:2000 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
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